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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/507,132	09/10/2004	Koichiro Kaku	1254-0258PUS1	2346

2292 7590 10/18/2007

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EXAMINER	
RAMIREZ, DELIA M	

ART UNIT	PAPER NUMBER
1652	

NOTIFICATION DATE	DELIVERY MODE
10/18/2007	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

mailroom@bskb.com

Office Action Summary	Application No.	Applicant(s)	
	10/507,132	KAKU ET AL.	
	Examiner	Art Unit	
	Delia M. Ramirez	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 August 2007*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-21* is/are pending in the application.

4a) Of the above claim(s) *4 and 7-9* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,5,6,10,11,14-16 and 18-21* is/are rejected.

7)☒ Claim(s) *12,13 and 17* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *10 September 2004* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☒ Other: alignment

DETAILED ACTION

Status of the Application

Claims 1-21 are pending.

Applicant's amendment of claims 1-3, 5-6, 10-11, addition of claims 12-21, and submission of a new abstract as submitted in a communication filed on 8/7/2007 is acknowledged.

New claims 12-21 are directed to the elected subject matter and find support in the specification as indicated by Applicant. This application contains claims 4, 7-9 drawn to an invention non-elected with traverse in a communication filed on 11/17/2006. A complete reply to the final rejection must include cancellation of non-elected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01. Claims 1-3, 5-6, 10-21 are at issue and are being examined herein.

Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

Claim Objections

1. Claims 12 and 17 (claim 13 dependent thereon) is objected to due to the recitation of "comprising of the amino acid sequence". This should be amended to recite "comprising the amino acid sequence". Appropriate correction is required.

Claim Rejections - 35 USC § 112, Second Paragraph

2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

3. Claims 1-3, 5-6, 10-11, 14, 19-21 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. This rejection is necessitated by amendment.

4. Claims 1, 5, 19 (claims 2, 3, 6, 20-21 dependent thereon) are indefinite in the recitation of "protein consisting of an amino acid sequence wherein said amino acid sequence is obtained by deletion, substitution or addition of one or more amino acids in SEQ ID NO: 2, wherein the amino acid at position 75 is methionine..." and "protein consisting of an amino acid sequence wherein said amino acid sequence is obtained by deletion, substitution or addition of 1-30 amino acids in SEQ ID NO: 2, wherein the amino acid at position 75 is methionine..." for the following reasons. As written, the term "wherein the amino acid at position 75 is methionine" is unclear and confusing because the term is meaningless in the absence of a reference sequence to which position 75 belongs. Since the protein required can be any variant of the polypeptide of SEQ ID NO: 2, and is not limited to a single modification which substitutes the amino acid at position 75 of SEQ ID NO: 2 to a methionine, one cannot determine if position 75 refers to position 75 in any variant of the polypeptide of SEQ ID NO: 2, or if the term is intended to encompass any variant of the polypeptide of SEQ ID NO: 2 wherein said variant differs from the polypeptide of SEQ ID NO: 2 by at least one substitution at position 75 of SEQ ID NO: 2, wherein the amino acid at position 75 of SEQ ID NO: 2 has been substituted with a methionine. For examination purposes, no patentable weight will be given to the term. Thus, it will be assumed that the claims read "protein consisting of an amino acid sequence wherein said amino acid sequence is obtained by deletion, substitution or addition of one or more (1-30) amino acids in SEQ ID NO: 2, and wherein said protein has ....". Correction is required.

5. Claim 14 is indefinite in the recitation of "gene codes for...and hybridizes to a nucleotide sequence complementary to the nucleotide sequence of SEQ ID NO: 1 under stringent conditions for the following reasons. First, it is noted that as known in the art, a nucleotide sequence is a graphical representation of the order in which nucleotides are arranged in a nucleic acid molecule. Also, as known in the art, hybridization occurs between nucleic acid molecules. Thus, nucleic acids do not hybridize to sequences but rather to other nucleic acids. In addition, the term "complementary" is unclear because one

cannot determine which "complements" are encompassed by the term. Fragments of any size which are complementary to the polynucleotides recited can be considered as "complements". Applicants have not define the term "complement", as it relates to size, in the specification either. Furthermore, the term "stringent conditions" is indefinite absent a statement of the experimental conditions under which the hybridization reaction is performed. Nucleic acids which will hybridize under some conditions will not necessarily hybridize under different conditions. The art does not recognize a single set of experimental conditions as stringent and the specification provides several examples of conditions which are considered stringent. For examination purposes, no patentable weight will be given to the term "stringent conditions", and the term "a nucleotide sequence complementary...." will be interpreted as "the full length complement of the polynucleotide of SEQ ID NO: 1". Correction is required.

6. Claim 10 remains indefinite in the recitation of "a kit for assessing a rice blast fungus resistant to a scytalone dehydratase inhibitor .... a pair of primers designed to flank a nucleotide sequence coding for an amino acid corresponding to valine at position 75 in the amino acid shown in SEQ ID NO: 4" for the reasons of record.

7. Applicant argues that the amino acid at position 75 of a mutant SCDH derived from the fungus of interest is an identifier. Thus, the kit of claim 10 only has to identify the amino acid at position 75. Applicant submits that the nucleotide sequence in claim 10 need not code for the entire amino acid sequence of a mutant SCDH derived from the fungus of interest.

8. Applicant's arguments have been fully considered but are not deemed persuasive. The Examiner acknowledges that (1) position 75 in the polypeptide of SEQ ID NO: 4 appears to be a marker for resistance to a scytalone dehydratase inhibitor in rice blast fungus, and (2) the preamble indicates the intended use for the kit. However, the claim as written, does not provide any link between assessing this resistance and the primers to be used, or how they are going to be used to assess this resistance. The claim as written does not require the sample to be tested with the primers to contain a nucleic acid

encoding a scytalone dehydratase or a fragment of a scytalone dehydratase. Since the claim does not require the nucleotide sequence to be flanked by the primers to encode (1) a scytalone dehydratase, or (2) a fragment of a scytalone dehydratase, and the primers are only required to flank a nucleic acid encoding a single amino acid (i.e., valine), it is unclear as to how one could ever assess whether a rice blast fungus is resistant to a scytalone dehydratase inhibitor, if the primers' target nucleic acid is unrelated to a scytalone dehydratase. It is reiterated herein that as written, the reference to SEQ ID NO: 4 does not link the primers to a nucleic acid which is somehow associated with a scytalone dehydratase. For examination purposes, it will be assumed that the claim is directed to a kit comprising a pair of primers. Correction is required.

9. Claim 11 remains indefinite in the recitation of "a kit....comprising an oligonucleotide including a nucleotide sequence coding for an amino acid corresponding to valine at position 75 in the amino acid sequence shown in SEQ ID NO: 4" for the reasons of record. For examination purposes, it will be assumed that the claim is directed to a kit which comprises an oligonucleotide, wherein said oligonucleotide comprises a nucleotide sequence which encodes a valine residue. Correction is required.

10. Claims 20-21 are indefinite in the recitation of "which contains 1-20/1-10 of said deletions, substitutions or additions" for the following reasons. It is unclear if the term "1-20/1-10 deletions, substitutions or additions" is intended to mean "1-20/1-10 amino acids deleted, substituted or added" or if the term is merely indicating how many times (1-20/1-10) a deletion, a substitution or an addition can be made. It is noted that if the term is intended to indicate how many times a deletion, substitution or addition can be made, each deletion/substitution/addition can delete/substitute/add any number of amino acids to the polypeptide of SEQ ID NO: 2. For examination purposes, it will be assumed that the claims read "the gene of claim 19, wherein said amino acid sequence is obtained by deletion, substitution or addition of 1-20/1-10 amino acids in SEQ ID NO: 2". Correction is required.

Claim Rejections - 35 USC § 112, First Paragraph

11. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

12. Claims 1-3, 5-6, 10-11 remain rejected and new claims 14-16 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This rejection as it relates to claims 14-16 is necessitated by amendment.

13. Applicant argues that claim 1 has been amended to require position 75 to be methionine and that the protein has scytalone dehydratase activity in the presence of a scytalone dehydratase inhibitor. Thus, the present invention is not directed to any nucleic acid encoding just any scytalone dehydratase and kits comprising primers having any structure.

14. Applicant's arguments have been fully considered but are not deemed persuasive to overcome the rejection or avoid the rejection of new claims 14-16. For the reasons extensively discussed above and in the previous Office action, the kits of claims 10-11 still require a genus of primers/oligonucleotides having essentially any structure. New claim 14 as interpreted is directed to the gene of claim 1 with the added limitation that said gene can hybridize under any conditions to the nucleic acid of SEQ ID NO: 1. Claim 15 is directed to the gene of claim 1 with the added limitation that said gene hybridizes to the nucleic acid of SEQ ID NO: 1 under conditions of 10-300 mM Na+ and a temperature range of 25-70 °C. Claim 16 is directed to the gene of claim 1 with the added limitation that said gene hybridizes to the nucleic acid of SEQ ID NO: 1 under conditions of 20-100 mM Na+ and a temperature range of 42-55 °C.

The genus of polynucleotides recited encompass species which are essentially structurally unrelated. Even the genus of nucleic acids recited in claims 15-16 encompass nucleic acids which are structurally diverse. A calculation of the Tm of the polynucleotides recited in claims 15-16 shows that

under the hybridization conditions recited, the claimed polynucleotides can be approximately 31.7% sequence identical to the polynucleotide of SEQ ID NO: 1 (claim 15, 300 mM Na+ and 25 °C) or 56.6% sequence identical to the polynucleotide of SEQ ID NO: 1 (claim 16, 100 mM Na+ and 42 °C). Using the well known equation of Meinkoth and Wahl (Current Protocols in Molecular Biology, Hybridization Analysis of DNA Blots, pages 2.10.8-2.10.11, 1993), Tm = 81.5 °C +16.6x$\log_{10}$[Na+] +0.41x(%GC) - .61x(%form) – 500/L, the corresponding Tm for the polynucleotide recited in claim 15 is approximately 93.3 °C assuming a G+C content of 50% and neglecting the term 500/L (93.3 °C = 81.5 + 16.6x$\log_{10}$[300/100] +0.41x(%50) - .61(%form = 0)). As known in the art, Tm is reduced by approximately 1 °C for each 1% mismatching, therefore under the conditions recited (300 mM Na+ and 25 °C), a wash at 25 °C is equivalent to approximately 68.3% mismatching (68.3% = 93.3°C – 25 °C). This level of mismatching amounts to 353 nucleotides which can be modified (353 = 0.683x516) within SEQ ID NO: 1. A similar calculation with hybridization conditions of 100 mM Na+ and 42 °C result in a level of mismatching of approximately 43.4% (43.4% = 85.4 °C - 42 °C), which amounts to approximately 224 nucleotides that can be modified within SEQ ID NO: 1. Thus, the genus of polynucleotides recited can potentially encompass polynucleotides encoding proteins which have almost no sequence identity to the polypeptide of SEQ ID NO: 2 since the nucleotide mismatches can potentially alter a similar number of codons.

As previously indicated, the specification is completely silent as to which amino acids can be added/deleted/substituted such that a variant of the polypeptide of SEQ ID NO: 2 would display scytalone dehydratase activity and be enzymatically active in the presence of an inhibitor. With regard to the genus of nucleic acids of claims 14-16, the specification is completely silent with regard to the structural features which are required in nucleic acids that hybridize under the conditions recited such that they would encode proteins having the recited activity. While the specification discloses the substitution of the amino acid at position 75 of the polypeptide of SEQ ID NO: 4 with a methionine to obtain a variant

scytalone dehydratase that is enzymatically active in the presence of an inhibitor, neither the specification nor the art discloses whether all scytalone dehydratases have a valine residue at a position corresponding to position 75 of SEQ ID NO: 4, and whether substituting the amino acid residue at a position corresponding to position 75 of SEQ ID NO: 4 with a methionine residue would result in an enzyme having the desired activity. Thus, for the reasons extensively discussed in the previous Office action and those set forth above, one cannot reasonably conclude that the claimed invention is adequately described by the teachings of the specification.

15. Claims 1-3, 5-6, 10-11 remain rejected and new claims 14-16, 18-20 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a nucleic acid encoding the polypeptide of SEQ ID NO: 2, vectors and isolated host cells comprising said nucleic acids, does not reasonably provide enablement for (1) any gene encoding any scytalone dehydratase, wherein said scytalone dehydratase is active in the presence of a scytalone dehydratase inhibitor, or in the presence of carpropamid, (2) any vector or transformant comprising the gene of (1), (3) kits comprising primers having any structure, (4) kits comprising any oligonucleotide encoding a valine residue, or (5) any non-isolated host cell or transgenic multicellular organism comprising a nucleic acid encoding the polypeptide of SEQ ID NO: 2. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims. This rejection as it relates to new claims 14-16, 18-20 is necessitated by amendment.

16. Applicant argues that claim 1 has been amended to require position 75 to be methionine and that the protein has scytalone dehydratase activity in the presence of a scytalone dehydratase inhibitor. Thus, the present invention is not directed to any nucleic acid encoding just any scytalone dehydratase and kits

comprising primers having any structure. Applicant asserts that only some and not undue experimentation is required in making and using the claimed invention.

17. Applicant's arguments have been fully considered but are not deemed persuasive to overcome the rejection or avoid the rejection of new claims 14-16, 18-21. As indicated above, the kits of claims 10-11 still require a genus of primers/oligonucleotides having essentially any structure. New claims 14-16 as interpreted are directed to the gene of claim 1 with the added limitation that said gene (1) can hybridize under any conditions to the nucleic acid of SEQ ID NO: 1, (2) under hybridization conditions of 10-300 mM Na+ and a temperature range of 25-70 °C, or (3) under hybridization conditions of 20-100 mM Na+ and a temperature range of 42-55 °C. In view of the fact that no patentable weight has been given to the term "position 75", claims 1-3, 5, 19-20 are directed to nucleic acids encoding a protein which is a variant of the polypeptide of SEQ ID NO: 2, wherein said variant (1) can comprise any structure, or (2) differs from the polypeptide of SEQ ID NO: 2 by having up to 20 or 30 amino acids deleted, substituted or added. See Claim Rejections under 35 USC 112, second paragraph, for claim interpretation. Claims 6 and 18 are directed in part to any transgenic multicellular organism comprising the nucleic acid of claim 1 or a nucleic acid encoding the polypeptide of SEQ ID NO: 2 in view of the fact that the term "transformant" is not limited to isolated host cells but also encompasses multicellular organisms. See prior Office action for discussion of the reasons why a transformant is not enabled by the teachings of the specification and/or the art.

As indicated above, in addition to those claims encompassing nucleic acids having any structure, claims 15-16 encompass nucleic acids which are structurally diverse and can potentially encompass scytalone dehydratases with little structural homology to the polypeptide of SEQ ID NO: 2. See written description rejection above for discussion of scope. While claims 19-20 encompass a large number of nucleic acids, neither the specification nor the art provide any teaching or suggestion as to which 20-30 amino acids in the polypeptide of SEQ ID NO: 2 can be substituted, deleted or added and obtain a variant

which has the desired activity. It is reiterated herein that the only modification taught by the specification wherein the desired activity is observed is a modification at position 75 of the polypeptide of SEQ ID NO: 4, replacing a valine residue for a methionine residue. The total number of variants of a polypeptide having a specific number of substitutions can be calculated from the formula $N!x19^{A}/(N-A)!/A!$, where N is the length in amino acids of the reference polypeptide and A is the number of allowed substitutions. Thus, for a variant of the polypeptide of SEQ ID NO: 2 having, for example, 20 amino acid substitutions, the total number of variants to be tested is $172!x19^{20}/(172-20)!/20!$ (SEQ ID NO: 2 has 172 amino acids) or $2.51x10^{51}$ variants. This number is greater as the number of substitutions increases. In view of the absence of information as to which structural elements in the polypeptide of SEQ ID NO: 2 or 4 are required and which ones can be modified to obtain a variant having the desired activity, one of skill in the art would have to test an essentially infinite number of variants to determine which ones display the desired activity. While enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, as is the case herein, the specification must provide a reasonable amount of guidance with respect to the direction in which the experimentation should proceed so that a reasonable number of species can be selected for testing. In view of the fact that such guidance has not been provided in the instant specification, it would require undue experimentation to enable the full scope of the claims.

Claim Rejections - 35 USC § 102

18. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

19. Claims 1-3, 5-6, 10-11 remain rejected and new claims 14-16, 19-21 are rejected under 35 U.S.C. 102(b) as being anticipated by Motoyama et al. (Biosci. Biotechnol. Biochem. 62(3):564-566,

1998; cited in the IDS) as evidenced by Nakasako et al. (Biochemistry 37:9931-9939, 1998; cited in the IDS). This rejection as it relates to claims 14-16, 19-21 is necessitated by amendment.

20. Applicant requests reconsideration in view of the amendments made. Applicant submits that the instant reference does not teach that the resistance to a scytalone dehydratase inhibitor depends on the type of amino acid at position 75 of a mutant SCDH.

21. Applicant's arguments have been fully considered but are not deemed persuasive to overcome the rejection or avoid the rejection of claims 14-16 and 19-21. For the reasons extensively discussed above in Claim Rejections under 35 USC 112, second paragraph, no patentable weight has been given to the term "position 75". Thus, claims 1-3, 5-6, 10-11, 14 as interpreted are directed to (1) a nucleic acid encoding a scytalone dehydratase which is active in the presence of a scytalone dehydratase inhibitor, or in the presence of carpropamid, (2) any vector or transformant comprising the nucleic acid of (1), (3) kits comprising primers having any structure, and (4) kits comprising any oligonucleotide encoding a valine residue. Claims 15-16, 19-21 as interpreted are directed in part to a nucleic acid encoding a scytalone dehydratase which is active in the presence of a scytalone dehydratase inhibitor, wherein the nucleic acid (1) hybridizes under hybridization conditions of 100 mM Na+ and 42 °C, or (2) encodes the polypeptide of SEQ ID NO: 2 except for one amino acid substitution. The scytalone dehydratase of Motoyama et al. is identical to the polypeptide of SEQ ID NO: 2 except for one amino acid substitution at position 75. See attached alignment. The hybridization conditions recited are equivalent to a percent identity of approximately 56.6% to SEQ ID NO: 1. See calculations shown above. Thus, the nucleic acid of Motoyama et al. would hybridize under the conditions recited in claims 14-16. In view of the fact that the polypeptide of Motoyama et al. is identical to the polypeptide of SEQ ID NO: 2 except for one amino acid substitution, the nucleic acid of Motoyama et al. anticipate claims 20-21. Thus, the teachings of Motoyama et al. anticipate the instant claims as written.

Allowable Subject Matter

22. The subject matter of claims 12-13 and 17 appears to be allowable over the prior art of record.

Conclusion

23. No claim is in condition for allowance.

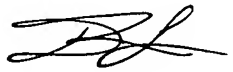
24. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

25. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PMR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

26. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM. If attempts to reach the examiner by telephone

are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571) 272-1600.



Delia M. Ramirez, Ph.D.
Primary Patent Examiner
Art Unit 1652

DR
October 9, 2007

16	528	56.1	122	2	Q8NJH8_9PEZI	Q8njh8 ophiostoma
17	526	55.8	168	1	SCYD_ASPFU	O14434 aspergillus
18	522	55.4	122	2	Q8NJI4_9PEZI	Q8nji4 ophiostoma
19	516	54.8	122	2	Q8NJI3_9PEZI	Q8nji3 ophiostoma
20	503	53.4	121	2	Q8NJH9_9PEZI	Q8njh9 ophiostoma
21	427	45.3	161	2	Q4I8I1_GIBZE	Q4i8i1 gibberella
22	332	35.2	1201	2	Q5BH35_EMENI	Q5bh35 aspergillus
23	99.5	10.6	605	2	Q8ZSD9_ANASP	Q8zsd9 anabaena sp
24	92	9.8	185	2	Q5YQ84_NOCFA	Q5yq84 nocardia fa
25	91	9.7	168	2	Q9RB47_9CLOT	Q9rb47 clostridium
26	90	9.6	318	2	Q7TDF4_9VIRU	Q7tdf4 halovirus h
27	89.5	9.5	583	2	Q6BVC7_DEBHA	Q6bvc7 debaryomyce
28	88.5	9.4	530	2	Q2UUC3_ASPOR	Q2uuc3 aspergillus
29	88	9.3	166	1	BAIE_EUBSP	P19412 eubacterium
30	87.5	9.3	333	2	Q5WYB7_LEGPL	Q5wyb7 legionella
31	87	9.2	211	2	Q3IE87_PSEHT	Q3ie87 pseudoalter
32	87	9.2	286	2	Q3G8U4_9FIRM	Q3g8u4 syntrophomo
33	87	9.2	924	1	LOXC1_ORYSA	P38419 oryza sativ
34	87	9.2	941	1	LOXC2_ORYSA	Q84yk8 oryza sativ
35	87	9.2	1277	2	Q2UED8_ASPOR	Q2ued8 aspergillus
36	86.5	9.2	331	2	Q5X6W7_LEGPA	Q5x6w7 legionella
37	86.5	9.2	331	2	Q5ZXE8_LEGPH	Q5zxe8 legionella
38	86	9.1	201	2	Q2IS89_RHOPA	Q2is89 rhodopseudo
39	84.5	9.0	380	2	O26444_METTH	O26444 methanobact
40	84	8.9	349	1	WNT7B_MOUSE	P28047 mus musculu
41	84	8.9	349	2	Q5NSW6_RAT	Q5nsw6 rattus norv
42	84	8.9	353	2	Q6NZR1_MOUSE	Q6nzr1 mus musculu
43	84	8.9	441	2	Q4IDL7_GIBZE	Q4idl7 gibberella
44	84	8.9	1058	2	Q4X125_ASPFU	Q4x125 aspergillus
45	83.5	8.9	468	2	Q7R5D9_GIALA	Q7r5d9 giardia lam

ALIGNMENTS

RESULT 1
SCYD_MAGGR
ID SCYD_MAGGR STANDARD; PRT; 172 AA.
AC P56221;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Scytalone dehydratase (EC 4.2.1.94).
GN Name=Sdh1;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98233280; PubMed=9571787;
RA Motoyama T., Imanishi K., Yamaguchi I.;
RT "cDNA cloning, expression, and mutagenesis of scytalone dehydratase
RT needed for pathogenicity of the rice blast fungus, Pyricularia
RT oryzae.";
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RN [2]
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RA Lindqvist Y., Jordan D.B.;
RT "High-resolution structures of scytalone dehydratase-inhibitor
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CC -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC scytalone they are two dehydration steps and one reduction step to
CC yield melanin.
CC -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC H(2)O.
CC -!- PATHWAY: Fungal melanin biosynthesis; first step.
CC -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC in the central part of the hydrophobic core of the monomer, which
CC functions independently.
CC --

CC --
DR EMBL; AB004741; BAA34046.1; -; mRNA.
DR PDB; 1IDP; X-ray; A/B/C=1-172.
DR PDB; 1STD; X-ray; @=1-172.
DR PDB; 2STD; X-ray; @=1-172.
DR PDB; 3STD; X-ray; A/B/C=10-172.
DR PDB; 4STD; X-ray; A/B/C=10-172.
DR PDB; 5STD; X-ray; A/B/C=10-172.
DR PDB; 6STD; X-ray; A/B/C=10-172.
DR PDB; 7STD; X-ray; A/B/C=10-172.
DR LinkHub; P56221; -.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.

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DR   ProDom; PD022193; Scytalone_DH; 1.
KW   3D-structure; Lyase; Melanin biosynthesis.
FT   CHAIN         1    172       Scytalone dehydratase.
FT                                /FTId=PRO_0000097639.
FT   HELIX        13     32
FT   TURN         33     33
FT   HELIX        35     39
FT   TURN         40     41
FT   STRAND       42     49
FT   HELIX        51     54
FT   STRAND       55     55
FT   STRAND       57     62
FT   HELIX        63     71
FT   STRAND       72     72
FT   TURN         73     76
FT   TURN         79     80
FT   STRAND       81     83
FT   STRAND       86     96
FT   TURN         97     98
FT   STRAND       99    115
FT   TURN        116    117
FT   STRAND      121    138
FT   TURN        139    140
FT   STRAND      141    155
SQ   SEQUENCE   172 AA;  20250 MW;  2FA56296D5EE00DC CRC64;

  Query Match           99.6%;  Score 938;  DB 1;  Length 172;
  Best Local Similarity  99.4%;  Pred. No. 3e-77;
  Matches  171;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 2
Q6XR11_9PEZI
ID   Q6XR11_9PEZI   PRELIMINARY;   PRT;   186 AA.
AC   Q6XR11;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Syctalone dehydratase I.
GN   Name=SD1;
OS   Ceratocystis resinifera.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=95837;
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